-continued

<213> ORGANISM: Artificial Sequence
<220> FEATURE:
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<400> SEQUENCE: 4

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We claim:

1. A method for determining the number of repeat units in a repeat region of a target nucleic acid comprising the steps of:

(A) contacting a plurality of different-sequence primers with a polynucleotide sample under conditions effective for said primers to anneal to primer-complementary regions in one or more target polynucleotides, to form one or more target-primer hybrid(s), wherein either (1) each different-sequence primer contains (i) a target binding segment and (ii) a tag segment having a nucleotide sequence that uniquely identifies the target binding segment, or (2) one or more polynucleotides in the sample are tagged polynucleotides that contain a tag segment having a nucleotide sequence that uniquely identifies the attached polynucleotide,

(B) performing a first primer extension reaction on said hybrid(s) using a first primer extension reagent;

(C) separating the target-primer hybrid(s) and unreacted first primer extension reagent;

(D) performing a second primer extension reaction on said hybrid(s) using a second primer extension reagent, wherein at least one of the first or second primer extension reagents includes an extendible nucleotide having a label attached thereto;

(E) separating the target-primer hybrid(s) from unreacted second primer extension reagent;

(F) measuring a signal produced by the label;

(G) treating the label so as to render the label undetectable; and

(H) repeating a cycle of steps (A) through (G) until the signal detected in the target-primer hybrid(s) is substantially less than a signal detected in a previous cycle, wherein prior to step (F), at least an aliquot of either (1) said different-sequence primers or (2) said tagged sample polynucleotides are contacted with an addressable array of immobilized, different tag complements, and each different tag complement contains a sequence that is complementary to one of said tag segments, under conditions effective to hybridize the tag segments to corresponding tag complements on the support.

2. The method of claim 1 wherein step (D) further includes reacting the target-primer hybrid(s) with a primer termination reagent.

3. The method of claim 1 wherein each different-sequence primer contains (i) a target binding segment and (ii) a tag segment having a nucleotide sequence that uniquely identifies the target binding segment.

4. The method of claim 3 wherein the contacting in step (I) is performed prior to step (A).

5. The method of claim 3 wherein the contacting in step (I) is performed after step (A).

6. The method of claim 3 wherein said method is performed on at least two replicate arrays, and one of the replicate arrays is subjected to at least one more cycle of steps (A) through (G) than is a second replicate array.

7. The method of claim 1 wherein one or more polynucleotides in the sample are tagged polynucleotides that contain a tag segment having a nucleotide sequence that uniquely identifies the attached polynucleotide.

8. The method of claim 7 wherein the contacting in step (I) is performed prior to step (A).

9. The method of claim 7 wherein the contacting in step (I) is performed after step (A).

10. The method of claim 7 wherein said method is performed on at least two replicate arrays, and one of the replicate arrays is subjected to at least one more cycle of steps (A) through (G) than is a second replicate array.

11. The method of claim 1 wherein the label is selected from the group consisting of fluorescent and chemiluminescent molecules.

12. The method of claim 1 wherein the label is attached to the extendible nucleotide through a cleavable linker.

13. The method of claim 1 wherein the target nucleic acid is amplified prior to analysis.

14. The method of claim 13 wherein amplification is achieved using a PCR.

15. The method of claim 1 wherein the step of treating the label so as to render the label undetectable includes cleaving the label from the labeled extendible nucleotide.

16. The method of claim 1 wherein the step of treating the label so as to render the label undetectable includes destroying a signal-producing property of the label.

17. A method for determining the number of repeat units in a repeat region of a target nucleic acid comprising the steps of:

(A) contacting a plurality of different-sequence primers with a polynucleotide sample under conditions effective for said primers to anneal to primer-complementary regions in one or more target polynucleotides, to form one or more target-primer hybrid(s), wherein either (1) each different-sequence primer contains (i) a target binding segment and (ii) a tag segment having a nucleotide sequence that uniquely identifies the target binding segment, or (2) one or more polynucleotides in the sample are tagged polynucleotides that contain a tag segment having a nucleotide sequence that uniquely identifies the attached polynucleotide,

(B) performing a first primer extension reaction on said hybrid(s) using a first primer-extension reagent;

(C) separating the target-primer hybrid(s) from unreacted first primer extension reagent;

(D) performing a second primer extension reaction on said hybrid(s) using a second primer extension reagent and with a primer termination reagent, the primer termination reagent including a nucleotide terminator having a label attached thereto;

(E) separating the target-primer hybrid(s) from unreacted second primer extension reagent and unreacted primer termination reagent;

(F) measuring a signal produced by the label; and

(G) repeating a cycle of steps (A) through (F) until a signal is detected indicating incorporation of the nucleotide terminator,

wherein prior to step (F), at least an aliquot of either (1) said different-sequence primers or (2) said tagged sample polynucleotides are contacted with an addressable array of immobilized, different tag complements, and each different tag complement contains a sequence that is complementary to one of said tag segments, under conditions effective to hybridize the tag segments to corresponding tag complements on the support.

18. The method of claim **17** wherein each different-sequence primer contains (i) a target binding segment and (ii) a tag segment having a nucleotide sequence that uniquely identifies the target binding segment.

19. The method of claim **18** wherein the contacting in step (H) is performed prior to step (A).

20. The method of claim **18** wherein the contacting in step (H) is performed after step (A).

21. The method of claim **18** wherein said method is performed on at least two replicate arrays, and one of the replicate arrays is subjected to at least one more cycle of steps (A) through (F) than is a second replicate array.

22. The method of claim **17** wherein one or more polynucleotides in the sample are tagged polynucleotides that contain a tag segment having a nucleotide sequence that uniquely identifies the attached polynucleotide.

23. The method of claim **22** wherein the contacting in step (H) is performed prior to step (A).

24. The method of claim **22** wherein the contacting in step (H) is performed after step (A).

25. The method of claim **22** wherein said method is performed on at least two replicate arrays, and one of the replicate arrays is subjected to at least one more cycle of steps (A) through (F) than is a second replicate array.

26. The method of claim **17** wherein the label is selected from the group consisting of fluorescent and chemiluminescent molecules.

27. The method of claim **17** wherein the target nucleic acid is amplified prior to analysis.

28. The method of claim **27** wherein amplification is achieved using a PCR.

29. A kit useful for determining the number of repeat units in a repeat region of a target nucleic acid comprising:

a plurality of different-sequence primers, each containing (i) a target binding segment and (ii) a tag segment having a nucleotide sequence that uniquely identifies the target binding segment,

a first primer extension reagent; and

a second primer extension reagent, wherein at least one of the first or second primer extension reagents includes an extendible nucleotide having a label attached thereto.

30. The kit of claim **29**, which further includes an addressable array of immobilized, different tag complements, wherein each different tag complement contains a sequence that is complementary to one of said primer tag segments, under conditions effective to hybridize the tag segments to corresponding tag complements on the support.

31. The kit of claim **29** wherein the label is selected from the group consisting of fluorescent and chemiluminescent molecules.

32. The kit of claim **29** wherein the label is attached to the extendible nucleotide through a cleavable linker.

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